

# Package ‘healthyFlowData’

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**Type** Package

**Title** Healthy dataset used by the flowMatch package

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**Description** A healthy dataset with 20 flow cytometry samples used by the flowMatch package.

**License** Artistic-2.0

**biocViews** FlowCytometryData

**Depends** R (>= 2.15.0), flowCore

**Imports** methods

**git\_url** <https://git.bioconductor.org/packages/healthyFlowData>

**git\_branch** RELEASE\_3\_19

**git\_last\_commit** 324f6aa

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